

Resource Summary Report

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Biostrings

RRID:SCR_016949

Type: Tool

Proper Citation

Biostrings (RRID:SCR_016949)

Resource Information

URL: <https://bioconductor.org/packages/release/bioc/html/Biostrings.html>

Proper Citation: Biostrings (RRID:SCR_016949)

Description: Software package for efficient manipulation of biological strings. Memory efficient string containers, string matching algorithms, and other utilities, for fast manipulation of large biological sequences or sets of sequences.

Resource Type: sequence analysis software, software resource, data analysis software, software application, data processing software

Keywords: manipulation, biological, string, memory, efficient, container, sequence, set, DNA, RNA, protein

Funding:

Availability: Free, Available for download, Freely available

Resource Name: Biostrings

Resource ID: SCR_016949

Alternate URLs:

https://web.stanford.edu/class/bios221/labs/biostrings/lab_1_biostrings.html

License: Artistic 2.0

Record Creation Time: 20220129T080332+0000

Record Last Update: 20250521T061656+0000

Ratings and Alerts

No rating or validation information has been found for Biostrings.

No alerts have been found for Biostrings.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 148 mentions in open access literature.

Listed below are recent publications. The full list is available at [FDI Lab - SciCrunch.org](#).

Carré A, et al. (2025) Interferon- γ promotes HLA-B-restricted presentation of conventional and alternative antigens in human pancreatic γ -cells. *Nature communications*, 16(1), 765.

Johnston J, et al. (2024) Metatranscriptomic Analysis Reveals Synergistic Activities of Comammox and Anammox Bacteria in Full-Scale Attached Growth Nitrogen Removal System. *Environmental science & technology*, 58(29), 13023.

Subramani PG, et al. (2024) Conserved role of hnRNPL in alternative splicing of epigenetic modifiers enables B cell activation. *EMBO reports*, 25(6), 2662.

Chivu AG, et al. (2024) Evolution of promoter-proximal pausing enabled a new layer of transcription control. *bioRxiv : the preprint server for biology*.

Shutt-McCabe J, et al. (2024) The plasmid-borne hipBA operon of *Klebsiella michiganensis* encodes a potent plasmid stabilization system. *Journal of applied microbiology*, 135(10).

Garreau M, et al. (2024) Chemical modification patterns for microRNA therapeutic mimics: a structure-activity relationship (SAR) case-study on miR-200c. *Nucleic acids research*, 52(6), 2792.

Chamberlin JT, et al. (2024) Differences in molecular sampling and data processing explain variation among single-cell and single-nucleus RNA-seq experiments. *Genome research*, 34(2), 179.

Naderi J, et al. (2024) An activity-specificity trade-off encoded in human transcription factors. *Nature cell biology*, 26(8), 1309.

Zaccaron AZ, et al. (2024) Transcriptome analysis of two isolates of the tomato pathogen *Cladosporium fulvum*, uncovers genome-wide patterns of alternative splicing during a host infection cycle. *PLoS pathogens*, 20(12), e1012791.

Esposito F, et al. (2024) Safe and effective liver-directed AAV-mediated homology-independent targeted integration in mouse models of inherited diseases. *Cell reports. Medicine*, 5(7), 101619.

Mätlik K, et al. (2024) Cell-type-specific CAG repeat expansions and toxicity of mutant Huntingtin in human striatum and cerebellum. *Nature genetics*, 56(3), 383.

Holm JB, et al. (2024) SpeciateIT and vSpeciateDB: Novel, fast and accurate per sequence 16S rRNA gene taxonomic classification of vaginal microbiota. *bioRxiv : the preprint server for biology*.

Immonen TT, et al. (2024) No evidence for ongoing replication on ART in SIV-infected macaques. *Nature communications*, 15(1), 5093.

Hillung J, et al. (2024) Accumulation Dynamics of Defective Genomes during Experimental Evolution of Two Betacoronaviruses. *Viruses*, 16(4).

Patel L, et al. (2024) Single-base resolution quantitative genome methylation analysis in the model bacterium *Helicobacter pylori* by enzymatic methyl sequencing (EM-Seq) reveals influence of strain, growth phase, and methyl homeostasis. *BMC biology*, 22(1), 125.

Pflughaupt P, et al. (2024) Towards the genomic sequence code of DNA fragility for machine learning. *Nucleic acids research*, 52(21), 12798.

Yan Q, et al. (2024) Antibodies utilizing VL6-57 light chains target a convergent cryptic epitope on SARS-CoV-2 spike protein and potentially drive the genesis of Omicron variants. *Nature communications*, 15(1), 7585.

Carey-Fung O, et al. (2024) Discovery of a conserved translationally repressive upstream open reading frame within the iron-deficiency response regulator IDEF2. *BMC plant biology*, 24(1), 891.

Watts ME, et al. (2023) Circular RNAs arising from synaptic host genes during human neuronal differentiation are modulated by SFPQ RNA-binding protein. *BMC biology*, 21(1), 127.

Carré A, et al. (2023) Interferon- γ promotes neo-antigen formation and preferential HLA-B-restricted antigen presentation in pancreatic β -cells. *bioRxiv : the preprint server for biology*.